



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/689,677 B
Source: IFWO
Date Processed by STIC: 5/14/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE).
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

101689,677B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 3-6 missing the <220> "Feature"
 *Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 05/14/2004

PATENT APPLICATION: US/10/689,677B

TIME: 16:08:12

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\05142004\J689677B.raw

5 <110> APPLICANT: Wyeth
 6 Wolfman, Neil
 7 Bouxsein, Mary
 9 <120> TITLE OF INVENTION: ActRIIB Fusion polypeptides and Uses Therefor
 11 <130> FILE REFERENCE: 08702.6093-00000
 W--> 12 <140> CURRENT APPLICATION NUMBER: 10/689,677B
 C--> 13 <141> CURRENT FILING DATE: 2003-10-22
 13 <150> PRIOR APPLICATION NUMBER: October 22, 2003
 W--> 14 <160> NUMBER OF SEQ ID: 6
 16 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

199 <210> SEQ ID NO: 3
 200 <211> LENGTH: 378
 201 <212> TYPE: PRT
 202 <213> ORGANISM: Artificial Sequence
 W--> 203 <220> FEATURE: - PLS insert this mandatory
 203 <223> OTHER INFORMATION: Chimera/Fusion
 205 <400> SEQUENCE: 3
 207 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 208 1 5 10 15
 210 Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu
 211 20 25 30
 213 Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
 214 35 40 45
 216 Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
 217 50 55 60
 219 Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
 220 65 70 75 80
 222 Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
 223 85 90 95
 225 Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe
 226 100 105 110
 228 Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val
 229 115 120 125
 230 Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp
 231 130 135 140
 233 Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys
 234 145 150 155 160
 236 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 237 165 170 175

Does Not Comply
 Corrected Diskette Needed

(pg. 1-4)

Numeric identifier, with NO
 response.

Please
 see item
 # 11 on
 error summary
 sheet.

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Input Set : A:\PTO.FG.txt

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239 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 240 180 185 190
 242 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 243 195 200 205
 245 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 246 210 215 220
 248 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 249 225 230 235 240
 251 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 252 245 250 255
 254 Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 255 260 265 270
 257 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 258 275 280 285
 260 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 261 290 295 300
 263 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 264 305 310 315 320
 266 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 267 325 330 335
 269 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 270 340 345 350
 272 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 273 355 360 365
 275 Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys
 276 370 375

278 <210> SEQ ID NO: 4

279 <211> LENGTH: 1134

280 <212> TYPE: DNA

281 <213> ORGANISM: Artificial Sequence

W--> 282 <220> FEATURE: - pls insert

282 <223> OTHER INFORMATION: Chimera/Fusion

EX 284 <400> SEQUENCE: 4

285 atgaaattct tagtcaacgt tgcccttggt tttatgggtcg tgtacatttc ttacatctat 60
 287 gcgactagtg ggcgtgggga ggctgagaca cgggagtgca tctactacaa cgccaactgg 120
 288 gagctggagc gcaccaacca gagcggcctg gagcgtgctg aaggcgagca ggacaagcgg 180
 290 ctgcactgct acgcctcctg gcgcaacagc tctggcacca tcgagctcgt gaagaagggc 240
 292 tgctggctag atgacttcaa ctgctacgat aggcaggagt gtgtggccac tgaggagAAC 300
 294 cccaggtgt acttctgctg ctgtgaaggc aacttctgca acgagcgtt cactcatttg 360
 296 ccagaggctg gggggcccgga agtcacgtac gagccacccc cgacagcccc caccggcggc 420
 298 cgcgagagcg acgacgacaa gacgcgttct agagacaaaa ctacacatg cccaccgtgc 480
 300 ccagcacctg aactcctggg gggaccgtca gtcttctctt tcccccaaa acccaaggac 540
 302 accctcatga tctcccgga ccttgaggtc acatgcgtgg tgggtggacgt gagccacgaa 600
 304 gacctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660
 306 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 720
 308 caccaggact ggctgaattg caaggagtac aagtgaagg tctccaacaa agccctccca 780
 310 gtcccacatg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840
 312 accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctgggtc 900
 314 aaaggttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC 960

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Input Set : A:\PTO.FG.txt

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316 aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctatagcaag 1020
318 ctccaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080
320 gaggctctgc acaaccacta cacgcagaag agcctctccc tgtccccgcc taaa 1134

322 <210> SEQ ID NO: 5

323 <211> LENGTH: 4

324 <212> TYPE: PRT

325 <213> ORGANISM: Artificial Sequence

W--> 326 ~~<220> FEATURE:~~ -pls insert

326 <223> OTHER INFORMATION: Linking Sequence, Gly-Ser repeat

OK E--> 328 <400> SEQUENCE: 5

330 Gly Ser Gly Ser

331 1

333 <210> SEQ ID NO: 6

334 <211> LENGTH: 4

335 <212> TYPE: PRT

336 <213> ORGANISM: Artificial Sequence

W--> 337 ~~<220> FEATURE:~~ -pls insert

337 <223> OTHER INFORMATION: Linking Sequence, Enterokinase Cleavage Site

OK E--> 339 <400> SEQUENCE: 6

341 Asp Asp Asp Lys

342 1

VERIFICATION SUMMARY

DATE: 05/14/2004

PATENT APPLICATION: US/10/689,677B

TIME: 16:08:13

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\05142004\J689677B.raw

L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:205 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3 ✓
L:282 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:284 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4 ✓
L:326 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:328 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5 ✓
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:339 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6 ✓